SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

IRIE, Reiko

<120> IgM PRODUCTION BY TRANSFORMED CELL AND METHOD OF QUANTIFYING THE SAME

<130> C1-A0223P

<150> US 60/487,333

<151> 2003-07-15

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<223>

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gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
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cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac 288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
85 90 95

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct 384
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc 432
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
130 135 140

cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg 480
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145 150 155 160

agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc 528
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
165 170 175

atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc 576
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
180 185 190

cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca 624
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser

195 200 205

cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac 672
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
210 215 220

gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg 720
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225 230 235 240

cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc 768
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
245 250 255

cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc 816
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
260 265 270

tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg 864
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
275 280 285

cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag 912
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
290 295 300

gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca 960
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
305 310 315 320

ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc 1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
325 330 335

cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg 1056
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
340 345 350

tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca 1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
355 360 365

tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg 1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
370 375 380

gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc 1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
385 390 395 400

cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac 1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

405 410 415

ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat 1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
420 425 430

gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac 1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
435 440 445

ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc 1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
450 455 460

ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg 1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
465 470 475 480

aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct 1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
485 490 495

ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc 1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
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ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca 1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
515 520 525

ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg 1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
530 535 540

aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc 1680
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545 550 555 560

aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc 1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
565 570 575

ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac 1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
580 585 590

tga 1779

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<212> PRT
<213> Homo sapiens

<400> 2

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20 25 30

Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
130 135 140

Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
145 150 155 160

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
165 170 175

Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
180 185 190

Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
195 200 205

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
210 215 220

Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
225 230 235 240

Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
245 250 255

Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
260 265 270

Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
275 280 285

Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
290 295 300

Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
305 310 315 320

Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
325 330 335

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
340 345 350

Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
355 360 365

Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
370 375 380

Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
385 390 395 400

Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

405 410 415

Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
420 425 430

Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
435 440 445

Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
450 455 460

Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
465 470 475 480

Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
485 490 495

Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
500 505 510

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
530 535 540

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545 550 555 560

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
565 570 575

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
580 585 590

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1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc 384
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115 120 125

aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc 432
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130 135 140

ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc 480
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145 150 155 160

ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg 528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
165 170 175

gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag 576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180 185 190

gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc 624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
195 200 205

aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat 672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt 720
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225 230 235 240

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<213> Homo sapiens

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Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115 120 125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130 135 140

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145 150 155 160

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
165 170 175

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
180 185 190

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
195 200 205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

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<211> 480

<212> DNA

<213> Homo sapiens

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<222> (1)..(480)

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gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96
Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
20 25 30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc 144
Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
35 40 45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192
Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
50 55 60

cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga 240
Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
65 70 75 80

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct 288
Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
85 90 95

aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336
Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
100 105 110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga 384
Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
115 120 125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432
Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
130 135 140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa 480
Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp

145 150 155

<210> 6

<211> 159

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
35 40 45

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
50 55 60

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
65 70 75 80

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
85 90 95

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
100 105 110

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
115 120 125

Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
130 135 140

Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
145 150 155

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<210> 8
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<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 8

aacatgctct ggccgagcca gtcg 24

<210> 9

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 9

gcaagtccag ccagagtgtt ttat 24

<210> 10

<211> 24

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<213> Artificial

<220>

<223> an artificially synthesized sequence

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ctgtccttgc tgtcctgctc tgtg 24

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<211> 33

<212> DNA

<213> Artificial

<220>

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<210> 12

<211> 32

<212> DNA

<213> Artificial

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<210> 13

<211> 32

<212> DNA

<213> Artificial

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<210> 14

<211> 30

<212> DNA

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<220>

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<400> 14

ggagcaggcg gccgcacttc tccctctaac 30

<210> 15

<211> 24

<212> DNA

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<223> an artificially synthesized sequence

<400> 15

accattgaga accagatttg tgta 24

<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 16

tgtgtagcac ttgtttctgt cata 24

<210> 17

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 17

atgaattcca ccatgaagaa ccatttgc 28

<210> 18

<211> 26

<212> DNA

<213> Artificial

<220>

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<400> 18

tatctagatt agtcaggata gcaggc 26

<210> 19

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1788)

<223>

<400> 19

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gtc cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag 96
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtc tca gct att agt ggt agt ggt tat acc aca tac tac gca 240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala
65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tat tac tgt gcc aaa aaa ccg ggg gac tat ggt tcg ggg agt tat tac 384
Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr
115 120 125

ctt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt 432
Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser
130 135 140

gca tcc gcc cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg 480
Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro
145 150 155 160

tcg gat acg agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt 528
Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu
165 170 175

ccc gac tcc atc act ttc tcc tgg aaa tac aag aac aac tct gac atc 576
Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile
180 185 190

agc agc acc cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca 624
Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala
195 200 205

gcc acc tca cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca 672

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr
210 215 220

gac gaa cac gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa 720
Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu
225 230 235 240

aag aac gtg cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc 768
Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser
245 250 255

gtc ttc gtc cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc 816
Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser
260 265 270

aag ctc atc tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg 864
Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val
275 280 285

tcc tgg ctg cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac 912
Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp
290 295 300

cag gtg cag gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg 960
Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val
305 310 315 320

acc agc aca ctg acc atc aaa gag agc gac tgg ctc agc cag agc atg 1008
Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met
325 330 335

ttc acc tgc cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg 1056
Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala
340 345 350

tcc tcc atg tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc 1104
Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala
355 360 365

atc ccc cca tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg 1152
Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu
370 375 380

acc tgc ctg gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc 1200
Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser
385 390 395 400

tgg acc cgc cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc 1248
Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser
405 410 415

gag agc cac ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc 1296

Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile
420 425 430

tgc gag gat gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc 1344
Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr
435 440 445

cac aca gac ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag 1392
His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
450 455 460

ggg gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg 1440
Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
465 470 475 480

gag cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg 1488
Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr
485 490 495

ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag 1536
Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
500 505 510

ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc 1584
Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
515 520 525

cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa 1632
Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
530 535 540

gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag 1680
Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
545 550 555 560

gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt 1728
Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
565 570 575

aaa ccc acc ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc 1776
Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
580 585 590

acc tgc tac tga 1788
Thr Cys Tyr
595

<210> 20
<211> 595
<212> PRT
<213> Homo sapiens

<400> 20

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr
115 120 125

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser

130 135 140

Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro
145 150 155 160

Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu
165 170 175

Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile
180 185 190

Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala
195 200 205

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr
210 215 220

Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu
225 230 235 240

Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser
245 250 255

Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser
260 265 270

Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val
275 280 285

Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp
290 295 300

Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val
305 310 315 320

Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met
325 330 335

Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala
340 345 350

Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala
355 360 365

Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu
370 375 380

Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser
385 390 395 400

Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser
405 410 415

Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile
420 425 430

Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr
435 440 445

His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
450 455 460

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
465 470 475 480

Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr
485 490 495

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
500 505 510

Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
515 520 525

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
530 535 540

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu

545 550 555 560

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
565 570 575

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
580 585 590

Thr Cys Tyr
595

<210> 21
<211> 726
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(726)
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<400> 21
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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

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ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct      96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
            20                  25                  30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt     144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
        35                  40                  45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag     192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50                  55                  60

aaa cca gga cag cct cct aag ttg ctc att tac tgg gca tct acc cgg     240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65                  70                  75                  80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat     288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat     336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
            100                 105                 110

tac tgt cag caa tat tat act act ctt ccg ctc act ttc ggc gga ggg     384
Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
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115 120 125

acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc 432
Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
130 135 140

ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg 480
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145 150 155 160

tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag 528
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
165 170 175

gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag 576
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
180 185 190

cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg 624
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
195 200 205

agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc 672
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
210 215 220

cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag 720

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu

225 230 235 240

tgt tag 726

Cys

<210> 22

<211> 241

<212> PRT

<213> Homo sapiens

<400> 22

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

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Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser

35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln

50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
115 120 125

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
130 135 140

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145 150 155 160

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
165 170 175

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
180 185 190

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
195 200 205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
210 215 220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225 230 235 240

Cys

<210> 23

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 23

caacaggcag gcaggggcag caag 24

<210> 24

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 24

agcataatta aagccaagga ggag 24

<210> 25

<211> 68

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 25

cctgatcatg aagacgtcga ctagtccgga tccccgggag ctcgagcgct ctagatcttt 60

aattaagg 68

<210> 26

<211> 76

<212> DNA

<213> Artificial

<220>

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<400> 26

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ttcatgatca ggccgg 76

<210> 27

<211> 23

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 27

gaggaattcc accatgaaga acc 23

<210> 28

<211> 27

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 28

gaggcggccg cttagtcagg atagcag 27

<210> 29

<211> 32

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 29

aaaagcggcc gcgatcataa tcagccatac ca 32

<210> 30

<211> 36

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 30

aaaactcgag aagcttagac atgataagat acattg 36

<210> 31

<211> 12

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized linker sequence

<400> 31

cccggatccg gg 12